

This Page Is Inserted by IFW Operations  
and is not a part of the Official Record

## **BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning documents *will not* correct images,  
please do not report the images to the  
Image Problem Mailbox.**

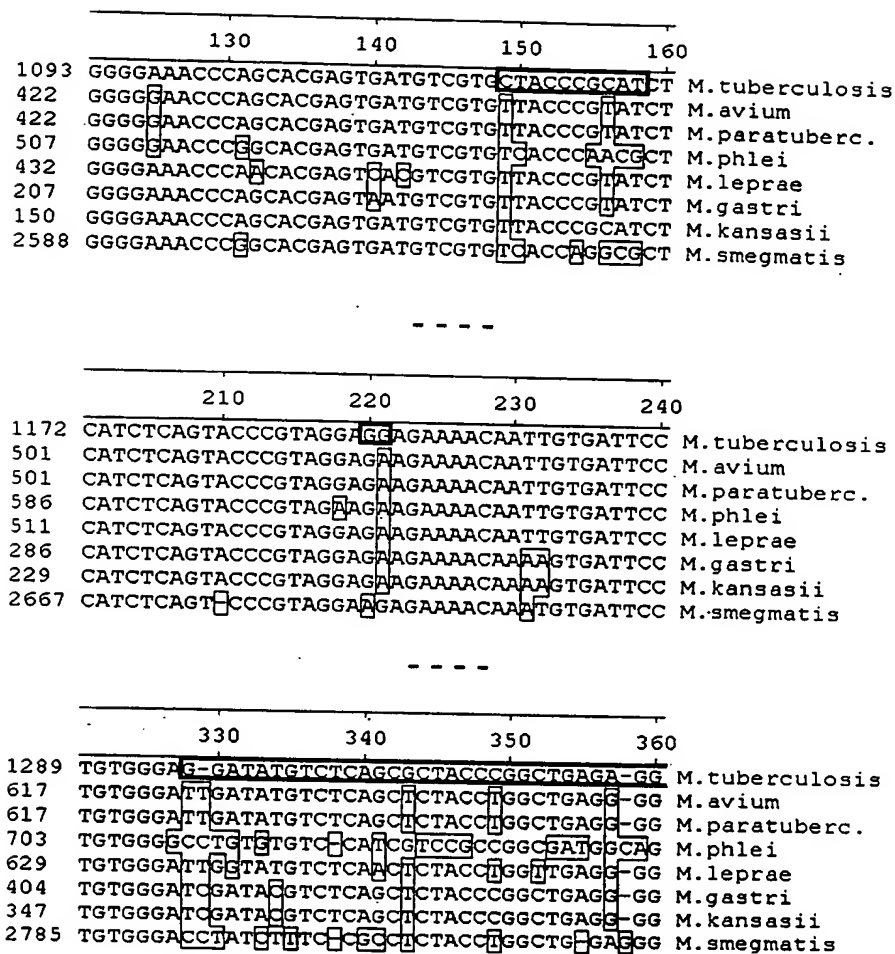


Figure 1A

	370	380	390	400	
1327	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.tuberculosis
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.avium
656	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.paratuberc.
742	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.phlei
668	TAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.leprae
443	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.gastri
386	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.kansasii
2823	CAGTCAGAAAGTGTCTGTTAGCGGAAGTGGCCTGGGAT				M.smegmatis
- - - -					
	450	460	470	480	
1406	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.tuberculosis
735	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.avium
735	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.paratuberc.
820	TGCTGCCGCTGTACAGG--TCCCGAGTAGCAGCGGGCC				M.phlei
747	TGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.leprae
522	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.gastri
465	CGGCACCTGCCTTATCAATTCCTGAGTAGCAGCGGGCC				M.kansasii
2902	CGACGTCTGCTTATGGTGTTCCTGAGTAGCAGCGGGCC				M.smegmatis
	490	500	510	520	
1446	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.tuberculosis
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.avium
775	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.paratuberc.
857	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.phlei
787	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.leprae
562	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.gastri
505	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.kansasii
2942	CGTGGAAATCGCTGTGAATCGCCGGGACCACCCGGTAAG				M.smegmatis

Figure 1B

	610	620	630	640	
1566	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCC	TCCT			M. tuberculosis
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. avium
894	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. paratuberc.
976	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. phlei
907	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. leprae
682	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. gastri
625	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. kansasii
3062	GTACCTGAAACCGTGTGCCTACAATCCGTCAGAGCCTCCT				M. smegmatis

	650	660	670	680	
1606	TTTCCTCTCCGGAGGAGGGT	GGTGATGGCGTGCCTTTTGA			M. tuberculosis
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. avium
934	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. paratuberc.
1016	CTT-----	GTGGGGTGATGGCGTGCCTTTTGA			M. phlei
947	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. leprae
722	T-----	GTGGGGTGATGGCGTGCCTTTTGA			M. gastri
665	C-----	GTGGGGTGATGGCGTGCCTTTTGA			M. kansasii
3102	ACGTGT-----	GTGGGGTGATGGCGTGCCTTTTGA			M. smegmatis

	690	700	710	720	
1646	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. tuberculosis
4	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. bovis
959	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. avium
23	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. intracellul.
959	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. paratuberc.
1046	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. phlei
972	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. leprae
747	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. gastri
690	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. kansasii
3132	AGAATGAGCCTGCGAGTCAGGGACATGTCGCAAGGTTAAC				M. smegmatis

Figure 1C

	770	780	790	800	
1726	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M.tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGAATAGTGGCGTGT				M.bovis
1039	CG	----	CATCCCC	TTTGGGGTGT	-----AGTGGCGTGT M.avium
103	CG	----	CATCCCC	TTTGGGGTGT	-----AGTGGCGTGT M.intracellular
1039	CG	----	CATCCCT	TTTGGGGTGT	-----AGTGGCGTGT M.paratuberc.
1126	CGTAT	CC	CAACTG	TTGGGGTGTGT	-----AGTGGTGTGT M.phlei
1052	CGTAT	---	CACG	TGTGAGCGTGT	-----AGTGGCGTGT M.leprae
827	CGTAT	---	CACGCGT	AGCGTGT	-----AGTGGCGTGT M.gastri
770	CGTAT	---	CGCGCG	AGCGTGT	-----AGTGGCGTGT M.kansasii
3212	CGTAT	---	CCACACA	AGTGTGTGT	-----AGTGGTGTGT M.smegmatis

	970	980	990	1000	
1926	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.tuberculosis
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.avium
1228	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.paratuberc.
1322	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.phlei
1244	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.leprae
1019	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.gastri
962	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.kansasii
3408	ATTTAGGTGCAGCGTTGCGTGGTTCACCGGGAGGTAGAG				M.smegmatis

	1050	1060	1070	1080	
2005	CAGCCAAACTCCGAATGCCG-TGGTG-TA-ATTCGTGGCA				M.tuberculosis
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.avium
1307	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.paratuberc.
1401	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.phlei
1323	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.leprae
1098	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.gastri
1041	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.kansasii
3486	CAGCCAAACTCCGAATGCCG-TGGTG-TATAAGCGTGGCA				M.smegmatis

Figure 1D

5/31

	1130	1140	1150	1160	
2082	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.tuberculosis		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.avium		
1385	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.paratuberc.		
1479	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.phlei		
1401	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.leprae		
1175	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.gastri		
1118	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.kansasii		
3566	ACAGCCCAGATCGCCGGCTAAGGCCCC	CAAGCGTGTGCTA	M.smegmatis		
-----					
	1290	1300	1310	1320	
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.tuberculosis		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.avium		
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.paratuberc.		
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.phlei		
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.leprae		
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.gastri		
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.kansasii		
3726	CTCAAGCACACCGCCGAAGCCGCGGCACAT	CCACCTTGT-	M.smegmatis		
	1330	1340	1350	1360	
2280	-GGTGGGTG	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.tuberculosis	
1583	GGGTGGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.avium	
1583	GGGTGGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.paratuberc.	
1676	TGGGTGGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.phlei	
1600	GGGTGGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.leprae	
1367	AGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.gastri	
1310	AGGT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.kansasii	
3764	TT	TGGGTAGGGGAGCGTCCCTCATT	CAGCGAAG	M.smegmatis	

Figure 1E

6/31

	1370	1380	1390	1400	
2319	CCAC	GGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. tuberculosis
1623	CT	CCGGGTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. avium
1623	CT	CCGGGTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. paratuberc.
1716	CCGCCG	GTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. phlei
1640	CCGCCG	GTGATCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. leprae
1402	CCGCCG	GTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. gastri
1345	CTGCCG	GTGACCGGTGGTGGAGGGTGGGGGAGTGAGAAT			M. kansasii
3796	CCGCCG	GTATCGAGTGGTGGAGGGTGGGGGAGTGAGAAT			M. smegmatis
	1410	1420	1430	1440	
2359	GCAGGCATGAGTAGCG	CAAGGCAAGTGAGAACCTTGCCC			M. tuberculosis
1662	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. avium
1662	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. paratuberc.
1756	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. phlei
1680	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. leprae
1442	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. gastri
1385	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. kansasii
3836	GCAGGCATGAGTAGCG	TAAGGCAAGTGAGAACCTTGCCC			M. smegmatis
- - - -					
	1570	1580	1590	1600	
2519	CGCCCCGTGAC	BAATCA-GCGGTACTAACCACCCAAAACCG			M. tuberculosis
1821	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. avium
1821	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. paratuberc.
1915	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. phlei
1840	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. leprae
1602	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. gastri
1545	CGCCCCGTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. kansasii
3996	CGTCCCTGAT	GAATCA-GCGGTACTAACCACCCAAAACCG			M. smegmatis

Figure 1F

	1610	1620	1630	1640	
2558	GAT-CGATCAC-TCCCCTTCGGGGG	TGTGGAGTTC-TGG			M.tuberculosis
1860	GAT-CGACCAT-TCCCCTTCGGGGG	GTGGCGATT-CGG			M.avium
1860	GAT-CGACCAT-TCCCCTTCGGGGG	GTGGCGATT-CGG			M.paratuberc.
1955	GCG-CGATC-ATCC-TTCGGGG	GTGACGGTTG-GG			M.phlei
1879	GAT-CGACCAT-TCCCCTTCGGGGG	TATGGAGGTT-CGG			M.leprae
1641	GAT-CGATCAC-TCCCCTTCGGGGG	GTGGAGGTC-TGG			M.gastri
1584	GAT-CGATCAC-TCCCCTTCGGGGG	GTGGAGGTC-TGG			M.kansasii
4035	ACCGTGACCCACCT-TTCGGGG	TGTGGCGTTGGTGG			M.smegmatis

	1650	1660	1670	1680	
2594	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.tuberculosis
1896	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.avium
1896	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.paratuberc.
1986	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.phlei
1917	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.leprae
1677	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.gastri
1620	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.kansasii
4071	GGCTGCGTGGGAACCTTCGCTGGTAGTAGTCAAGCGAA	GGG			M.smegmatis

	1690	1700	1710	1720	
2634	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.tuberculosis
1936	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.avium
1936	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.paratuberc.
2025	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.phlei
1957	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.leprae
1717	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.gastri
1660	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.kansasii
4111	-GTGACGCAGGAAGGTAGCCGTACCAGTCAGTGGTAATA-				M.smegmatis

Figure 1G



8/31

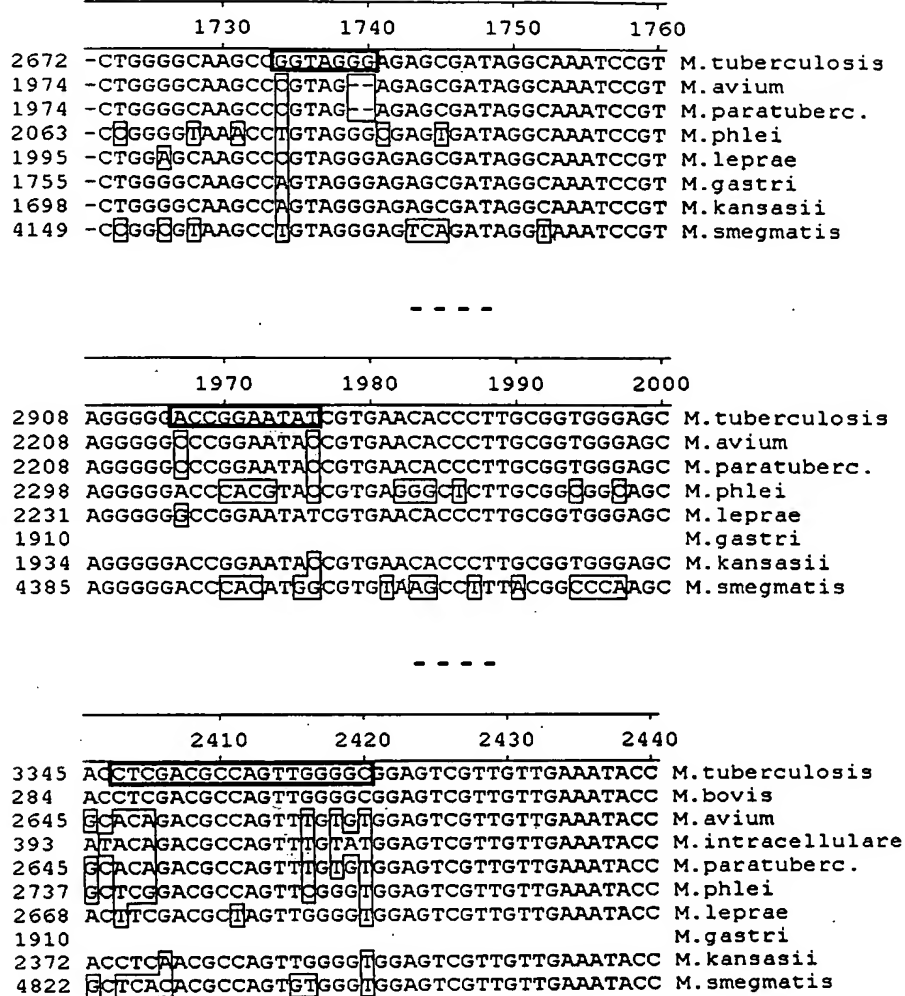


Figure 1H

9/31

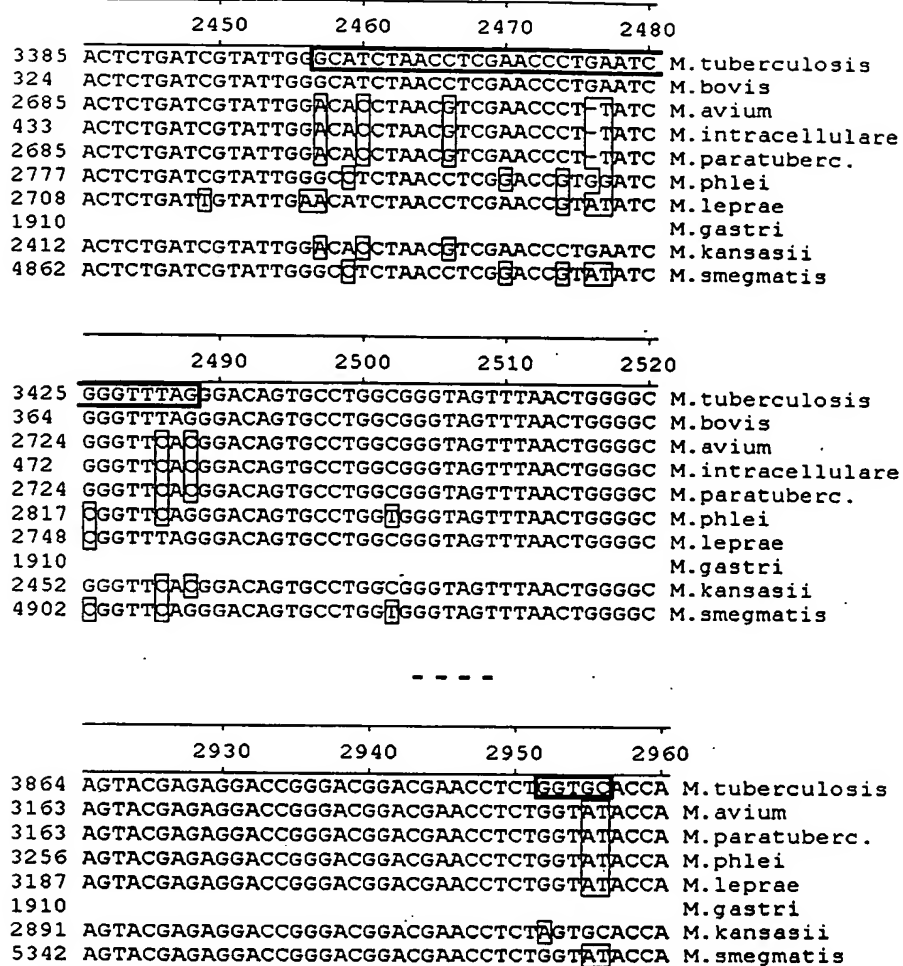


Figure 11

10/31

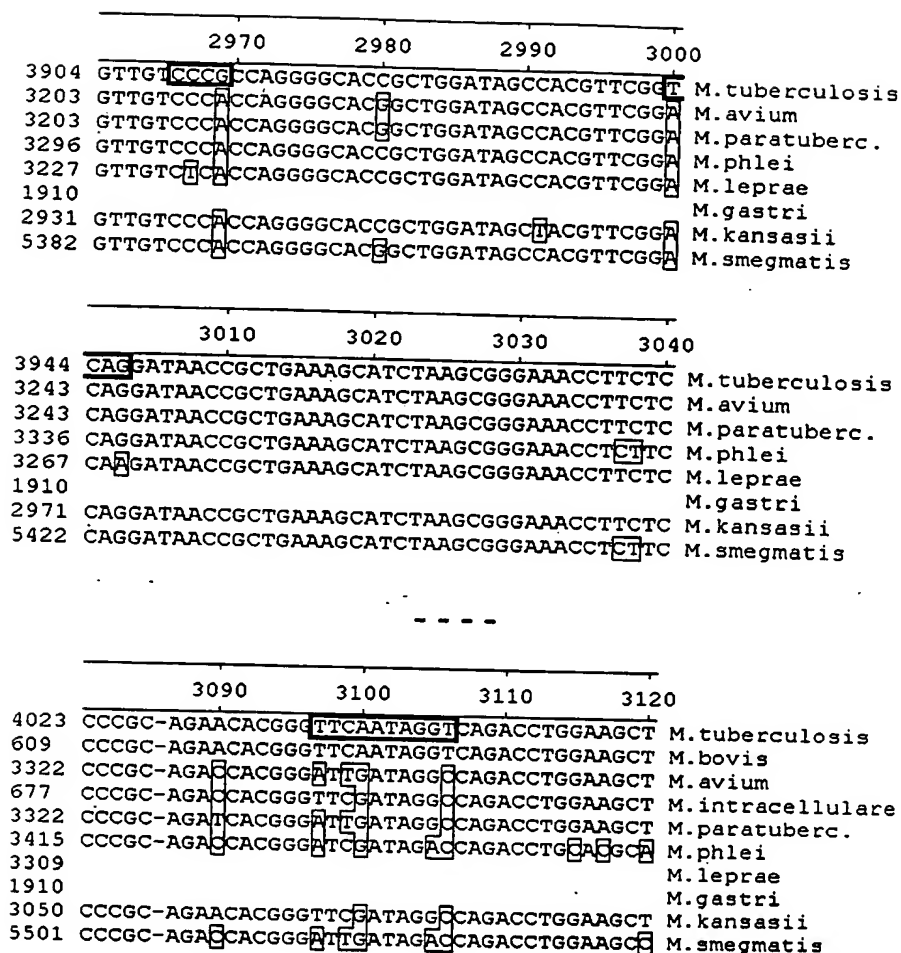


Figure 1J

	50	60	70	80	
2	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.tuberculosis
141	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.bovis
39	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.avium
1	-----TAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.intracellulare
39	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.paratuberc.
2	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.scrofulaceum
40	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.leprae
2	CGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.kansasii
2	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.gastri
40	GCGGCGTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.gordonae
1	-----GTGCTTAAACACATGCAAGTCGAACGGAAGG	GTCTC			M.marinum

	90	100	110	120	
42	T-----TCGGAGAT	ACTCGAGTGGCGAACGGGT			M.tuberculosis
181	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.bovis
79	T-----TCGGAGTACTCGAGTGGCGAACGGGT				M.avium
32	T-----TCGGG--TACTCGAGTGGCGAACGGGT				M.intracellulare
79	T-----TCGGAGTACTCGAGTGGCGAACGGGT				M.paratuberc.
42	T-----TCGGG--TACTCGAGTGGCGAACGGGT				M.scrofulaceum
80	TAAAAAATCTTTT	TAGAGATACTCGAGTGGCGAACGGGT			M.leprae
41	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.kansasii
42	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.gastri
80	-----G--G--TACTCGAGTGGCGAACGGGT				M.gordonae
36	T-----TCGGAGATACTCGAGTGGCGAACGGGT				M.marinum

	130	140	150	160	
70	GAGTAACACGTGGG	TGATCTGCCCTGCACTTC	GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	TGATCTGCCCTGCACTTC	GGGATAA		M.bovis
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.avium
59	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.intracellulare
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.paratuberc.
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.scrofulaceum
120	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.leprae
69	GAGTAACACGTGGG	CAATCTGCCCTGCACACC	GGGATAA		M.kansasii
70	GAGTAACACGTGGG	CAATCTGCCCTGCACACC	GGGATAA		M.gastri
104	GAGTAACACGTGGG	CAATCTGCCCTGCACATC	GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	GGGATAA		M.marinum

Figure 2A

12/31

	170	180	190	200	
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGAC	CACGGGA			M.tuberculosis
248	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.bovis
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.avium
98	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTTTAGG				M.intracellulare
146	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.paratuberc.
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.scrofulaceum
160	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCTCAAGA				M.leprae
108	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.kansasii
109	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.gastri
143	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACTTGG				M.gordonae
103	GCCTGGGAAACTGGGTCTAATACCGGATAGGACCACGGGA				M.marinum

	210	220	230	240	
149	TGCATGTCTTGTGGTGGAAAG	CGCTTTAG	CGGTGTGGGAT		M.tuberculosis
288	TGCATGTCTTGTGGTGGAAAGCGCTTTAGCGGTGTGGGAT				M.bovis
186	CGCATGTCTTGTGGTGGAAAGC	TTTT	ACGGTGTGGGAT		M.avium
138	CGCATGTCTTGTGGTGGAAAGC	TTTT	CGGTGTGGGAT		M.intracellulare
186	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.paratuberc.
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.scrofulaceum
200	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.leprae
148	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.kansasii
149	CGCATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gastri
183	CACATGTCTTGTGGTGGAAAGC	TTTT	GCGGTGTGGGAT		M.gordonae
143	TTCATGTCTTGTGGTGGAAAG	CTTT	GCGGTGTGGGAT		M.marinum

	250	260	270	280	
189	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.tuberculosis
328	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.bovis
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.avium
176	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.intracellulare
224	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.paratuberc.
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.scrofulaceum
239	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.leprae
186	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.kansasii
187	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gastri
221	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.gordonae
181	GAGCCCGCGGCCTATCAGCTTGTGGTGGGGTGACGGCCT				M.marinum

Figure 2B

	450	460	470	480	
389	AAACCTCTTTTACCATCGACGAAGGTCCGGGTT				M.tuberculosis
528	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCGG				M.bovis
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.avium
376	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.intracellulare
424	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.paratuberc.
387	AAACCTCTTTTACCATCGACGAAGGTCTCA---CTTTGTGG				M.scrofulaceum
439	AAACCTCTTTTACCATCGACGAAGGTCTGGGAATCTCTCGG				M.leprae
386	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTCTCTCTCGG				M.kansasii
387	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.gastri
420	AAACCTCTTTTACCATCGACGAAGGTCCGGGTTTCTCTCGG				M.gordonae
381	AAACCTCTTTTACCATCGACGAAGGTCTGGGTTTCTCTCGG				M.marinum

- - - -

	1130	1140	1150	1160	
1069	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.tuberculosis
1208	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.bovis
1104	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGCCAGGGGACTCGTGAGAG				M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1119	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCACGTAATGGTGGGGACTCGTGAGAG				M.marinum

- - - -

	1250	1260	1270	1280	
1189	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.tuberculosis
1328	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.bovis
1224	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.avium
1176	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.intracellulare
1218	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.paratuberc.
1184	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.scrofulaceum
1239	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.leprae
1186	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.kansasii
1187	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.gastri
1220	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.gordonae
1181	CAATGGCCGGTACAAAGGGCTGCGATGCCGCGAGGTTAAG				M.marinum

Figure 2C

	1290	1300	1310	1320	
1229	CGAATCCTTA- <b>A</b> AGCCGGTCTCAGTTCGGAT <b>C</b> GGGTCT				<i>M. tuberculosis</i>
1368	CGAATCCTTA-AAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. bovis</i>
1264	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGAT <b>C</b> GGGTCT				<i>M. avium</i>
1216	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGAT <b>C</b> GGGTCT				<i>M. intracellulare</i>
1258	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGAT <b>C</b> GGGTCT				<i>M. paratuberc.</i>
1224	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. scrofulaceum</i>
1279	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. leprae</i>
1226	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. kansasii</i>
1227	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. gastri</i>
1260	CGAATCCTTTTAAAGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. gordonae</i>
1221	CGAATCCTTT <b>A</b> AGCCGGTCTCAGTTCGGATCGGGGTCT				<i>M. marinum</i>

	1330	1340	1350	1360	
1268	GCAACTCGACCC <b>C</b> TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. tuberculosis</i>
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. bovis</i>
1304	GCAACTCGACCC <b>C</b> TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. avium</i>
1256	GCAACTCGACCC <b>C</b> TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. intracellulare</i>
1298	GCAACT <b>C</b> GACCC <b>A</b> TGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. paratuberc.</i>
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. scrofulaceum</i>
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. leprae</i>
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. kansasii</i>
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. gastri</i>
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. gordonae</i>
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				<i>M. marinum</i>

Figure 2D

	50	60	70	80	
128	TTCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.tuberculosis
39	TGCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.bovis
41	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.phlei
3559	TACCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.leprae
5743	TCCCGAACCCGGAAGCTAAGCCTGCCAGCGCCGATGATAC				M.smegmatis
	90	100	110	120	
168	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.tuberculosis
79	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.bovis
81	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.phlei
3599	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.leprae
5782	TGCCCTCCCGGG---TGGAAAAGTAGGACACCGCCGAAC				M.smegmatis

Figure 3



16/31

	90	100	110	120	
382	GGGAGCTGTCAACCGAGC	ATTGATCCGAGGATTTCCGAAT			M.avium
382	GGGAGCTGTCAACCGAGCATTGATCCGAGGATTTCCGAAT				M.paratuberc.
1053	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.tuberculosis
467	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.phlei
392	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.leprae
167	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.gastri
110	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.kansasii
2548	GGGAGCTGTCAACCGAGC	TTGGATCCGAGGATTTCCGAAT			M.smegmatis

-----

	170	180	190	200	
462	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.avium
462	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.paratuberc.
1133	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.tuberculosis
547	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.phlei
472	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.leprae
247	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.gastri
190	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.kansasii
2628	GAATATATAGGGTGCG-GGAGG	TAACGCGGGGAAGTGAAA			M.smegmatis

-----

	250	260	270	280	
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.avium
541	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.paratuberc.
1212	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.tuberculosis
626	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.phlei
551	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.leprae
326	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.gastri
269	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.kansasii
2706	-GTCAGTAGTGGCGAGCGAAC	-CGGAACA-GGCTAAACCG			M.smegmatis

Figure 4A

	290	300	310	320	
578	CATG	CATG	GACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. avium
578	CATG	CATG	GACA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. paratuberc.
1250	CATG	CATG	GTA	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. tuberculosis
664	CATG	CATG	TGATACCGGGT	GGGGTTGTGTGTGCGGGGT	M. phlei
590	CACA	CATG	TCTA	ACTAGGTAGGGGTTGTGTGTGCGGGGT	M. leprae
365	CACG	CATG	GTTG	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. gastri
308	CACG	CATG	GTTG	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. kansasii
2745	TATGA	CATG	TGAT	ACCGGGTAGGGGTTGTGTGTGCGGGGT	M. smegmatis

	330	340	350	360	
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	-GG M. avium
617	TGTGGG	ATTGATATG	TCTCAG	TCTACCTGGCTGAGG	-GG M. paratuberc.
1289	TGTGGG	AG	GATATGTCTCAG	CTACCTGGCTGAGG	-GG M. tuberculosis
703	TGTGGG	SCCTGT	TGTCTCAG	CTACCTGGCTGAGG	-GG M. phlei
629	TGTGGG	ATTG	TATGTCTCAG	CTACCTGGCTGAGG	-GG M. leprae
404	TGTGGG	ATTG	TATGTCTCAG	CTACCTGGCTGAGG	-GG M. gastri
347	TGTGGG	ATTG	TATGTCTCAG	CTACCTGGCTGAGG	-GG M. kansasii
2785	TGTGGG	ATTG	TATGTCTCAG	CTACCTGGCTGAGG	-GG M. smegmatis

	370	380	390	400	
656	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. avium
656	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. paratuberc.
1327	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. tuberculosis
742	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. phlei
668	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. leprae
443	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. gastri
386	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. kansasii
2823	TAGTCAGAAAGTGT	CGTGGTTAGCGGAAGTGGCCTGGG	ATC		M. smegmatis

Figure 4B

18/31

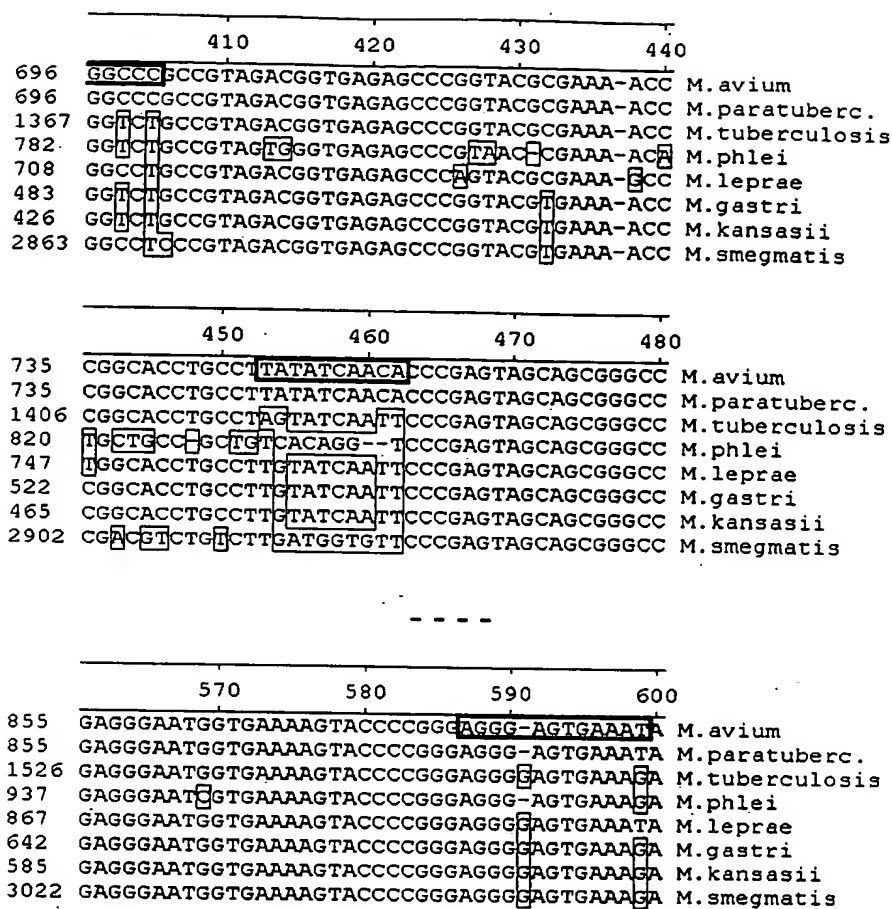


Figure 4C

19/31

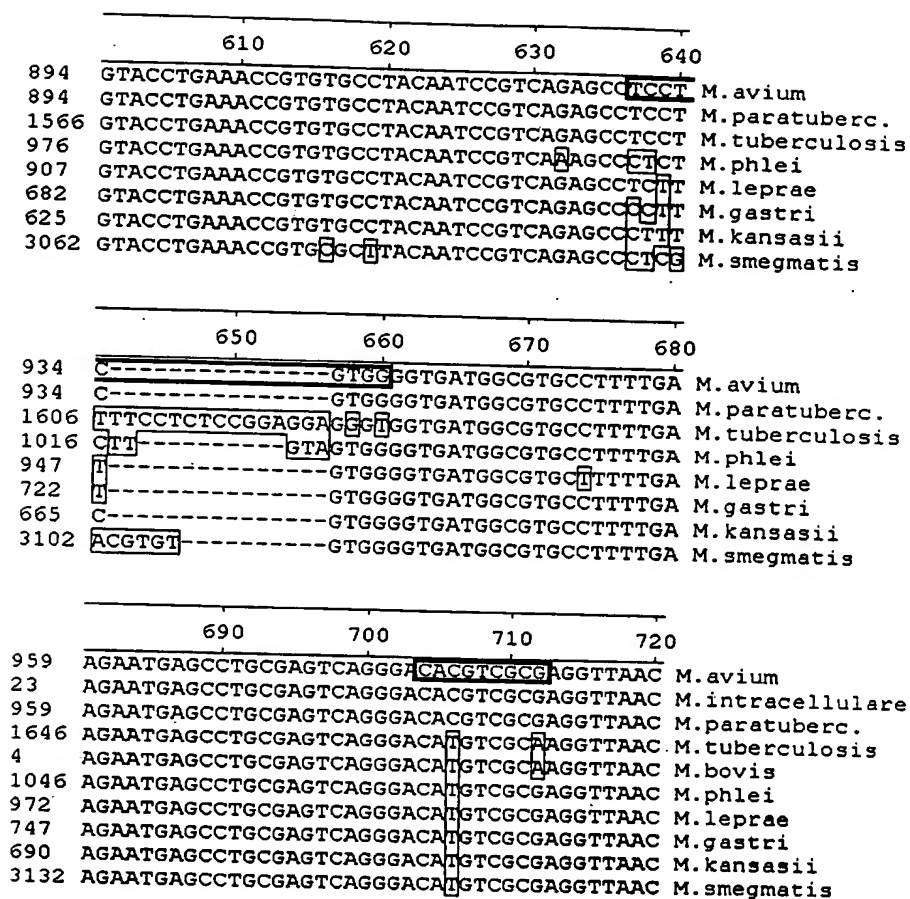


Figure 4D

	770	780	790	800	
1039	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. avium
103	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. intracellulare
1039	CGCATCCCCCTTGGG	-----	GTGTAGTGGCGTGT		M. paratuberc.
1726	CGACCCACACGCGCATACGCGCGTGTGA	TTAGTGGCGTGT			M. tuberculosis
84	CGACCCACACGCGCATACGCGCGTGTGA	TTAGTGGCGTGT			M. bovis
1126	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. phlei
1052	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. leprae
827	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. gastri
770	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. kansasii
3212	CGTATCCCAACCTGTT	-----	GGGGTTGGTGTAGTGGCGTGT		M. smegmatis

	1050	1060	1070	1080	
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. avium
1307	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. paratuberc.
2005	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. tuberculosis
1401	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. phlei
1323	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. leprae
1098	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. gastri
1041	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. kansasii
3486	CAGCCAAACTCCGAATGCCG	TGGTG-TAAAAGCGTGGCA			M. smegmatis

	1170	1180	1190	1200	
1425	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. avium
1425	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. paratuberc.
2122	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. tuberculosis
1519	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. phlei
1441	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. leprae
1215	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. gastri
1158	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. kansasii
3606	AGTGGAAAAGGATGTGTAGTCGCAGA	GACAACCAGGAGG			M. smegmatis

Figure 4E

	1250	1260	1270	1280	
1504	CTCACTGGTCAAGTGATT	ATGCGCC	GATAATGTAGCGGG		M.avium
1504	CTCACTGGTCAAGTGATT	ATGCGCCGATAATGTAGCGGG			M.paratuberc.
2201	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.tuberculosis
1598	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.phlei
1520	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.leprae
1294	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.gastri
1237	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.kansasii
3686	CTCACTGGTCAAGTGATT	TGCGCCGATAATGTAGCGGG			M.smegmatis

	1290	1300	1310	1320	
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.avium
1544	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.paratuberc.
2241	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.tuberculosis
1638	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.phlei
1560	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.leprae
1334	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.gastri
1277	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.kansasii
3726	CTCAAGCACACCGCCGAAGCCGCGGCACAT	TCATCTT-TA			M.smegmatis

	1330	1340	1350	1360	
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.avium
1583	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.paratuberc.
2280	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.tuberculosis
1676	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.phlei
1600	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.leprae
1367	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.gastri
1310	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.kansasii
3764	CGGTGGATGTGGGTAGGGGAGCGT	CCCC	CATTAGCGAAG		M.smegmatis

Figure 4F

22/31

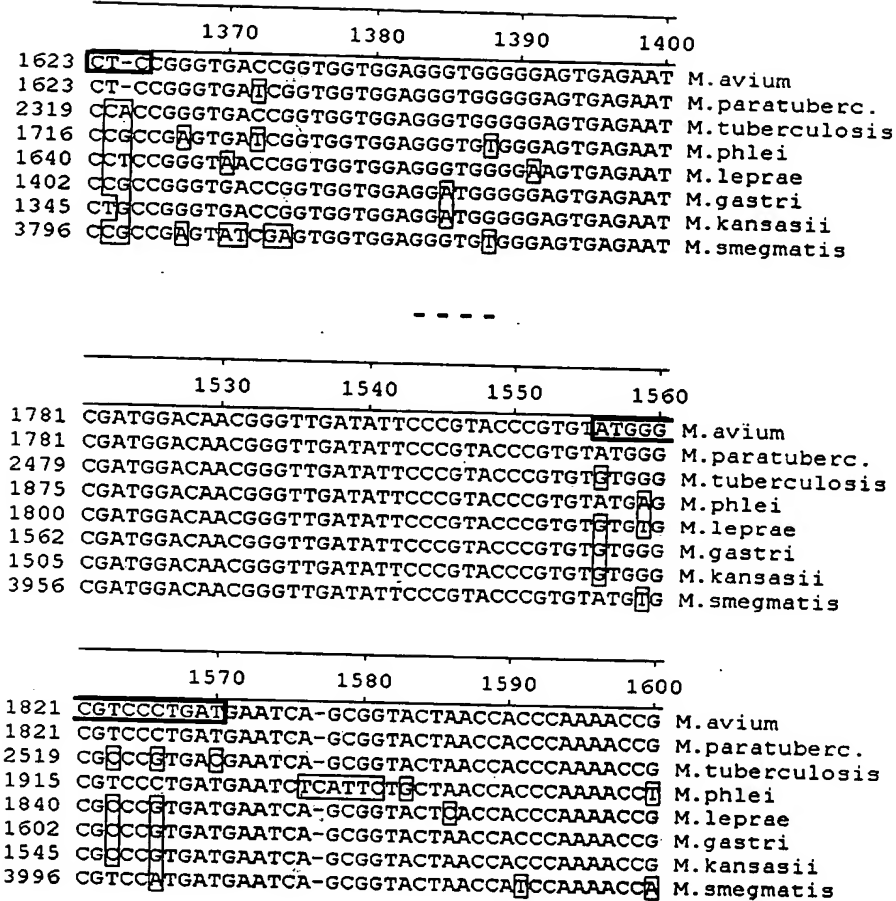


Figure 4G

	1610	1620	1630	1640	
1860	GAT-CGA	CCAT-T	CCCCTTCGGGGG	C-GTGGCGATT-CGG	M. avium
1860	GAT-CGACCAT	TCCCCTTCGGGGGC	GTGGCGATT-CGG		M. paratuberc.
2558	GAT-CGA	TCAC-TCCCCTTCGGGGG	TGTGGAGTTG	TGG	M. tuberculosis
1955	GAC-CGA	TC-TTCC-TTCGGGG	GTGGCGTTG	GG	M. phlei
1879	GAT-CGACCAT	TCCCCTTCGGGGGC	TATGGAGTT-CGG		M. leprae
1641	GAT-CGA	TCAC-TCCCCTTCGGGGGC	GTGGAGTTG	TGG	M. gastri
1584	GAT-CGA	TCAC-TCCCCTTCGGGGGC	GTGGAGTTG	TGG	M. kansasii
4035	ACCGTGACC	GCACCT-TTCCGGGG	TGTGGCGTTGGTGG		M. smegmatis

	1650	1660	1670	1680	
1896	GGCTGCGTGGG	GACCTTCGCTGGTAGTAGTCAAG	CAATGGG		M. avium
1896	GGCTGCGTGGG	GACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. paratuberc.
2594	GGCTGCGTGGG	GAACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. tuberculosis
1986	GGCTGCGTGGG	ACCG-GTGGTAGTAGTCAAGCAATGGG			M. phlei
1917	GGCTGCGTGGG	GAACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. leprae
1677	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. gastri
1620	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. kansasii
4071	GGCTGCGTGGG	ACCTTCGCTGGTAGTAGTCAAGCAATGGG			M. smegmatis

	1690	1700	1710	1720	
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. avium
1936	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. paratuberc.
2634	-GTGACGCAGGAAGGTAAGCCGTACCAGTCAGTGGTAATA-				M. tuberculosis
2025	-GTGACGCAGGAAGGTAAGCCGTACCAGTCAGTGGTAATA-				M. phlei
1957	-GTGACGCAGGAAGGTAAGCCGTACCAGTCAGTGGTAATA-				M. leprae
1717	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. gastri
1660	-GTGACGCAGGAAGGCAGCCGTACCAGTCAGTGGTAATA-				M. kansasii
4111	-GTGACGCAGGAAGGTAAGCCGTACCAGTCAGTGGTAATA-				M. smegmatis

	1730	1740	1750	1760	
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAATCCGT				M. avium
1974	-CTGGGGCAAGCCCGTAG--AGAGCGATAGGCAATCCGT				M. paratuberc.
2672	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. tuberculosis
2063	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. phlei
1995	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. leprae
1755	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. gastri
1698	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. kansasii
4149	-CTGGGGCAAGCCCGTAGGGAGAGCGATAGGCAATCCGT				M. smegmatis

Figure 4H



	1810	1820	1830	1840	
2051	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. avium
2051	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. paratuberc.
2751	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. tuberculosis
2141	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. phlei
2074	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. leprae
1834	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. gastri
1777	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. kansasii
4228	CG-AATTCGGT	GATCCTCTGCTGCCAAGAAAAGCCTCTA-			M. smegmatis

	1850	1860	1870	1880	
2089	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. avium
2089	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. paratuberc.
2789	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. tuberculosis
2179	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. phlei
2112	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. leprae
1872	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. gastri
1815	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. kansasii
4266	GCGAGC	ACATACGCGGCCGTACCCCAAACCAACACAGGT			M. smegmatis

- - - - -

	1970	1980	1990	2000	
2208	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. avium
2208	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. paratuberc.
2908	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. tuberculosis
2298	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. phlei
2231	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. leprae
1910					M. gastri
1934	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. kansasii
4385	AGGGGG	CCCGGAATACCGTGAACACCCTTGCGGTGGGAGC			M. smegmatis

	2010	2020	2030	2040	
2248	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. avium
2248	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. paratuberc.
2948	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. tuberculosis
2338	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. phlei
2271	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. leprae
1910					M. gastri
1974	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. kansasii
4425	GGGAT	TCGGTGCAGAAACCAAGTGGTAGCGACT-GTTTA			M. smegmatis

Figure 4I

	2130	2140	2150	2160	
2367	CCGTTAACC	GT--AAGGGTGAAGCGGAGAATTTAAGCCC			M.avium
2367	CCGTTAACC	CGT--AAGGGTGAAGCGGAGAATTTAAGCCC			M.paratuberc.
3067	CCGTTAACC	CG--AAGGGTGAAGCGGAGAATTTAAGCCC			M.tuberculosis
2457	CCGTTAACC	CTTCGGGGTGAAGCGGAGAATTTAAGCCC			M.phlei
2390	CTGTTAACC	CG--AAGGGTGAAGCGGAGAATTTAAGCCC			M.leprae
1910					M.gastri
2094	CCGTTAACC	CG--AAGGGTGAAGCGGAGAATTTAAGCCC			M.kansasii
4544	CCGTTAACC	CTTGGGGTGAAGCGGAGAATTTAAGCCC			M.smegmatis

-----

	2250	2260	2270	2280	
2485	GTAACGACTTC	CCAA--TGCTCTCAACCATAGACTCGGCGAA			M.avium
2485	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.paratuberc.
3185	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.tuberculosis
2577	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.phlei
2508	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.leprae
1910					M.gastri
2212	GTAACGACTTC	CAACTGTCTCAACCATAGACTCGGCGAA			M.kansasii
4663	GTAACGACTTC	CAACTGTCTCAAC--ATAGACTCGGCGAA			M.smegmatis

-----

	2370	2380	2390	2400	
2605	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.avium
2605	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.paratuberc.
3305	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.tuberculosis
2697	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.phlei
2628	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.leprae
1910					M.gastri
2332	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.kansasii
4782	GTTCCGTACGGTTTGTGTAGGATAGGTGGGAGACT	TTGAA			M.smegmatis

Figure 4J

26/31

	2410	2420	2430	2440	
2645	GCACGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. avium
393	ATACAGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. intracellulare
2645	GCACGACGCCAGTTTGTGTTGGAGTCGTTGTTGAAATACC				M. paratuberc.
3345	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. tuberculosis
284	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. bovis
2737	GCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. phlei
2668	ACCTCGACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. leprae
1910					M. gastri
2372	ACCTCAACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. kansasii
4822	GCTCAACGCCAGTTTGGGGGGAGTCGTTGTTGAAATACC				M. smegmatis
	2450	2460	2470	2480	
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. avium
433	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. intracellulare
2685	ACTCTGATCGTATTGGACACCTAACGTCGAACCT-TATC				M. paratuberc.
3385	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTTATC				M. tuberculosis
324	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTTATC				M. bovis
2777	ACTCTGATCGTATTGGGCTCTTAACCTCGAACCTTATC				M. phlei
2708	ACTCTGATCGTATTGGGCACTTAACCTCGAACCTTATC				M. leprae
1910					M. gastri
2412	ACTCTGATCGTATTGGACACCTAACGTCGAACCTTATC				M. kansasii
4862	ACTCTGATCGTATTGGGCTCTTAACCTCGAACCTTATC				M. smegmatis
- - - -					
	2690	2700	2710	2720	
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. avium
2924	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. paratuberc.
3625	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. tuberculosis
3017	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. phlei
2948	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. leprae
1910					M. gastri
2652	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. kansasii
5102	GGTGTCTCTCAACGGATAAAAGGTACCCCGGGGATAACAG				M. smegmatis
	2730	2740	2750	2760	
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. avium
2964	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. paratuberc.
3665	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. tuberculosis
3057	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. phlei
2988	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. leprae
1910					M. gastri
2692	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. kansasii
5142	GCTGATCTTCCCCAAGAGTCCATATCGACGGGATGGTTTG				M. smegmatis

Figure 4K

27/31

	2770	2780	2790	2800	
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. avium
3004	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. paratuberc.
3705	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. tuberculosis
3097	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. phlei
3028	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. leprae
1910					M. gastri
2732	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. kansasii
5182	GCACCTCGATGTCGGCTCGTCGCATCCTGGGGCTGGAGCA				M. smegmatis
	2810	2820	2830	2840	
3044	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. avium
3044	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. paratuberc.
3745	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. tuberculosis
3137	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. phlei
3068	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. leprae
1910					M. gastri
2772	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. kansasii
5222	GGTCCCAAGGGTTGGGCTGTTTCGCCC-ATTAAAGCGGCAC				M. smegmatis
- - - -					
	3050	3060	3070	3080	
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. avium
638	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. intracellulare
3283	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. paratuberc.
3984	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. tuberculosis
570	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. bovis
3376	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. phlei
3307	CAA				M. leprae
1910					M. gastri
3011	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. kansasii
5462	CAAGATCAGGTTT-CTCACCCCTTTTAGAGGGGATAAGGCC				M. smegmatis
	3090	3100	3110	3120	
3322	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. avium
677	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. intracellulare
3322	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. paratuberc.
4023	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. tuberculosis
609	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. bovis
3415	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. phlei
3309					M. leprae
1910					M. gastri
3050	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. kansasii
5501	CCCGC-AGACCACGGGATTGATAGGCACAGACCTGGAAGCT				M. smegmatis

Figure 4L

	130	140	150	160	
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.avium
59	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.intracellulare
107	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.paratuberc.
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.scrofulaceum
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.tuberculosis
209	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.bovis
120	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.leprae
69	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.kansasii
70	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gastri
104	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.gordonae
64	GAGTAACACGTGGG	CAATCTGCCCTGCACTTC	-GGGATAA		M.marinum
-----					
	450	460	470	480	
424	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.avium
376	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.intracellulare
424	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.paratuberc.
387	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.scrofulaceum
389	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.tuberculosis
528	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.bovis
439	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.leprae
386	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.kansasii
387	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.gastri
420	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.gordonae
381	AAACCTCTTTT	CACCATCGACGAAGGTCCGGG	TTTT	TCTCGG	M.marinum
	490	500	510	520	
429	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.tuberculosis
568	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.bovis
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.avium
416	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.intracellulare
464	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.paratuberc.
424	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.scrofulaceum
479	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.leprae
426	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.kansasii
427	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gastri
460	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.gordonae
421	ATTGACGGTAGGTGGAGAAGAAGC	ACCGGCCAACTACGTG			M.marinum

Figure 5A

29/31

	1130	1140	1150	1160	
1104	TCTCATGTTGCCAGC	GGGTAATGC	GGGGACTCGTGAGAG		M.avium
1056	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.intracellulare
1098	TCTCATGTTGCCAGCGGGTAATGC	GGGGACTCGTGAGAG			M.paratuberc.
1064	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.scrofulaceum
1069	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.tuberculosis
1208	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.bovis
1119	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.leprae
1066	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.kansasii
1067	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gastri
1100	TCTCATGTTGCCAGCGGGTAATGCCGGGGACTCGTGAGAG				M.gordonae
1061	TCTCATGTTGCCAGCAGTAATG	GGGGACTCGTGAGAG			M.marinum

- - - -

	1290	1300	1310	1320	
1264	CGAATCCTTTTAAGCCGGACTCAGTTCGGAT	GGGGTCT			M.avium
1216	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.intracellulare
1258	CGAATCCTTTTAAGCCGGACTCAGTTCGGATTGGGGTCT				M.paratuberc.
1224	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.scrofulaceum
1229	CGAATCCTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.tuberculosis
1368	CGAATCCTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.bovis
1279	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.leprae
1226	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.kansasii
1227	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.gastri
1260	CGAATCCTTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.gordonae
1221	CGAATCCTTTAAGCCGG	CTCAGTTCGGATTGGGGTCT			M.marinum

	1330	1340	1350	1360	
1304	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.avium
1256	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.intracellulare
1298	GCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCA				M.paratuberc.
1264	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.scrofulaceum
1268	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.tuberculosis
1407	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.bovis
1319	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.leprae
1266	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.kansasii
1267	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gastri
1300	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.gordonae
1260	GCAACTCGACCCCGTGAAGTCGGAGTCGCTAGTAATCGCA				M.marinum

Figure 5B

2550 | TTACGCGCGGCAGGACGAAAGACCCCGGGACCTTCACTA  
 2568 2569 |  
 2589 |

Mavium 23S:

Figure 6

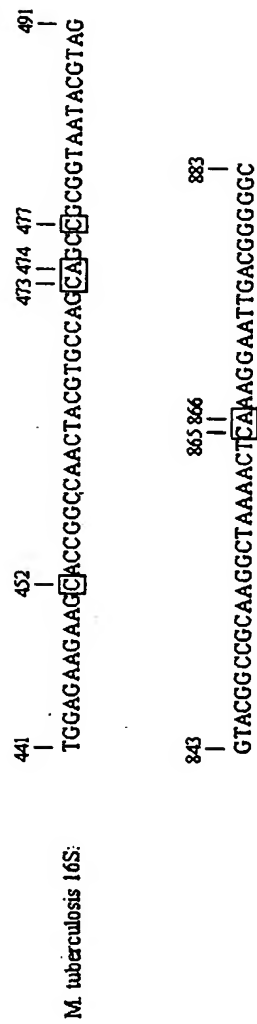


Figure 7